

EXPRESS MAIL
EL360933793US
ATTY. DKT. 266/187
SHEET 1 OF 11

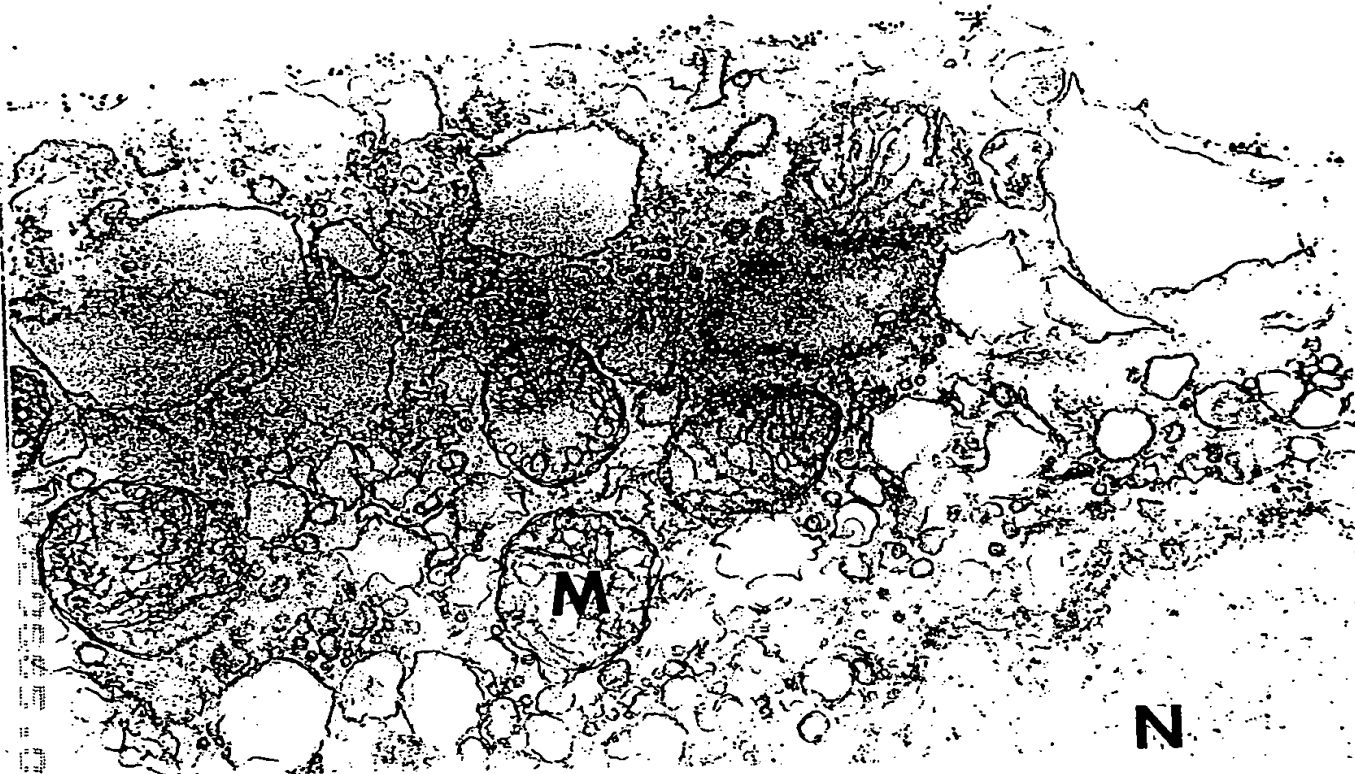


FIGURE 1

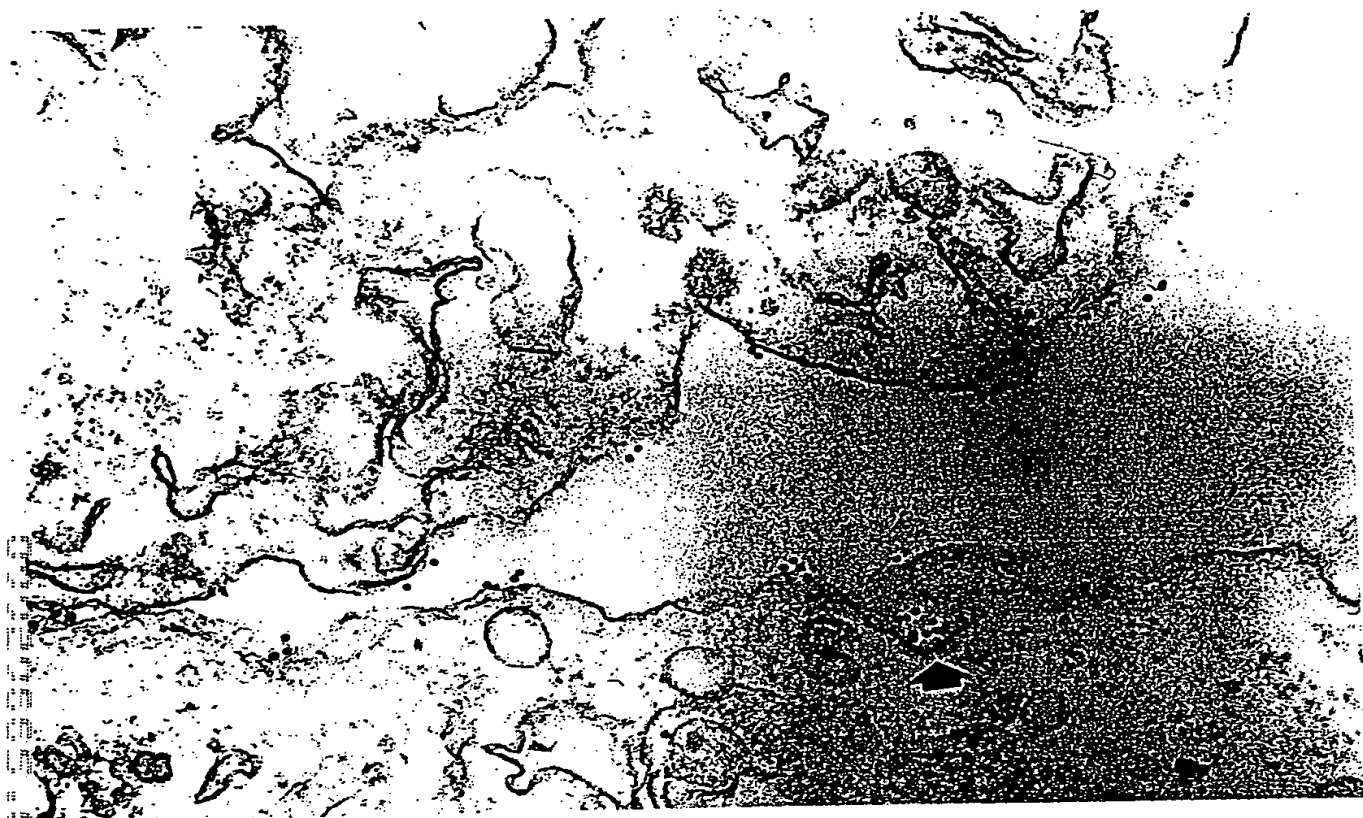


FIGURE 2

EXPRESS MAIL
EL360933793US
ATTY. DKT. 266/187
SHEET 3 OF 11



FIGURE 3

EXPRESS MAIL
EL360933793US
ATTY. DKT. 266/187
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FIGURE 4

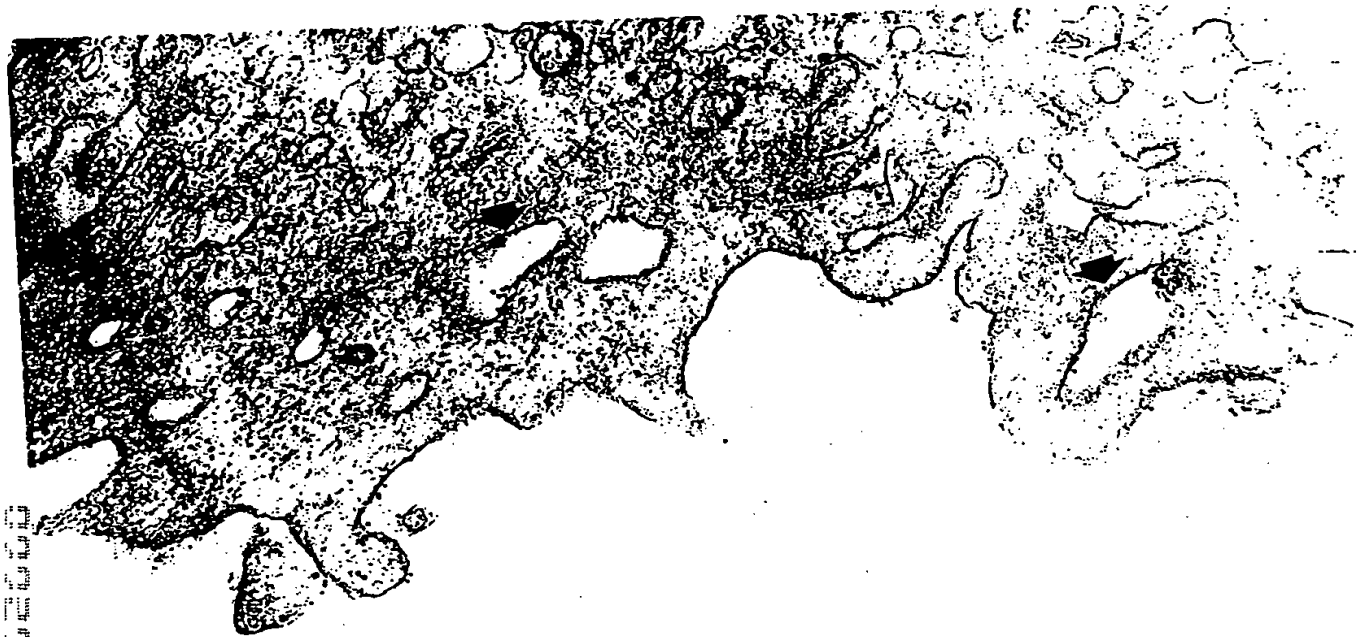


FIGURE 5

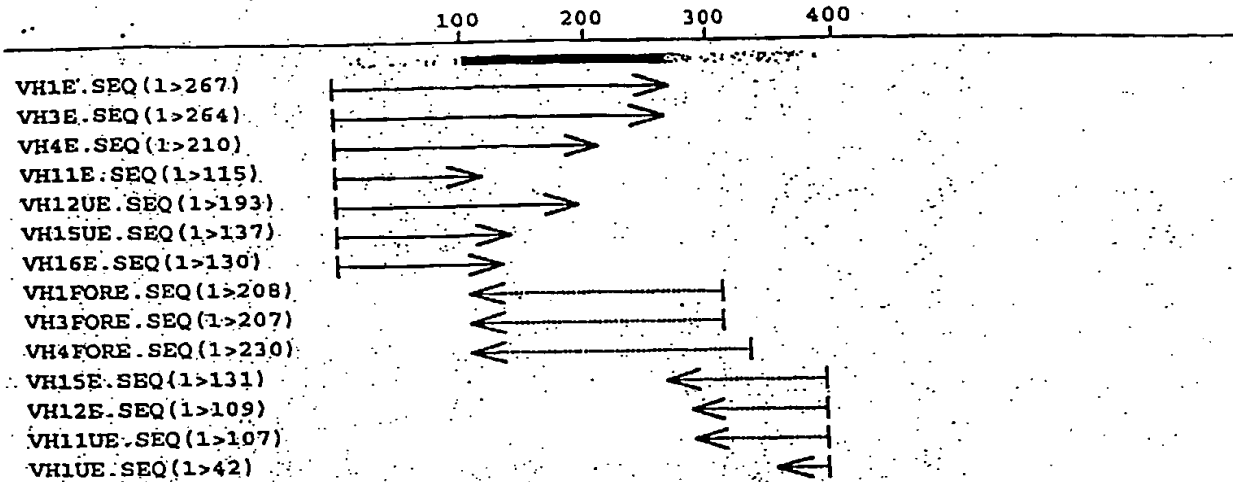


FIGURE 6

Enzymes: All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code

SEQ. ID. NO. 1
SEQ. ID. NO. 2
SEQ. ID. NO. 3
SEQ. ID. NO. 4
SEQ. ID. NO. 5

Pst I Dde I Ava II Alu I Pvu II Eco57 I Bsr I
Sau96 I
TCTCCTGT CAGGAAGTGCAGGTGCTCTCTCTGAGGTCCAGCTGCAACAGTCTGGACCTGAACTGGTGAAG 70
AGAGGACAGTCTCTGACGTCCACAGGAGAGACTCCAGGTGCGAGTGTGACAGCTGGACTTGACCACTTC
S P V R N C R C P L G P A A T V W T T G E
L L S G T A G V L S E V O L O S G P E L V K
L S C O E L O V S S L R S S C N S L O L N W S

SEQ. ID. NO. 1
SEQ. ID. NO. 2
SEQ. ID. NO. 3
SEQ. ID. NO. 4
SEQ. ID. NO. 5

Hph I Bsp6 II EcoRV Dra III Bsr I
CCTGGGACTTCAGTGAGGATATCCTGCAAGACTTCTGGATACACATTCAGTGAATATACCATACACTGGG 140
GGACCCTGAAGTCACTCCTATAGGACGTTCTGAAGACCTATGTGTAAGTGACTTATATGGTATGTGACCC
A W D F S E D I L O D F W I H I H I Y H T L G
P G T S V R I S C K T S G Y T F T E Y T I H W
L G L O G Y P A R L L D T H S L N I P Y T G

SEQ. ID. NO. 1
SEQ. ID. NO. 2
SEQ. ID. NO. 3
SEQ. ID. NO. 4
SEQ. ID. NO. 5

Hph I Nco I Rsa I Kpn I
TGAAGCAGAGCCATGGAAGAGCCTTGAGTGGATTGGAACATCAATCCTAACAATGGTGGTACCACCTA 210
ACTTCGTCCTCGGTACCTTTCTCGGAAGTCACTAACCTTTGTAGTTAGGATTGTTACCACCATGGTGGAT
E A E P W K E P V D W K H Q S O W W Y H L
V K O S H G K S L E W I G N I N P N N G G T T Y
S R A M E R A L S G L E T S I L T H V V P P

SEQ. ID. NO. 1
SEQ. ID. NO. 2
SEQ. ID. NO. 3
SEQ. ID. NO. 4
SEQ. ID. NO. 5

Taq I Hae III Acc I Bsr I Rsa I Alu I Ban II Sac I
CAATCAGAAGTTCGAGGACAAGGCCACATTGACTGTAGACAAGTCTCCAGTACAGCCTACATGGAGCTC 280
GTTAGTCTTCAAGCTCCTGTTCCGGTGTAAGTACATCTGTTCCAGGAGGTCATGTCGGATGTACCTCGAG
O S E V R G O G H I D C R O V L Q Y S L H G A
N O K F E D K A T L T V D K S S S T A Y M E L
T I R S S R T R P H L T S P P V O P T W S S

SEQ. ID. NO. 1
SEQ. ID. NO. 2
SEQ. ID. NO. 3
SEQ. ID. NO. 4
SEQ. ID. NO. 5

Dde I Hinf I Pst I Alu I Pvu II Sau96 I Bsr I Hae III
CGCAGCCTAACATCTGAGGATTCTCGAGTCTATTATTGTGCAGCTGGTTGGAACCTTTGACTAGTGGGGCC 350
CGGTCCGATTGTAGACTCCTAAGACGTCAGATAATAACACGTCGACCAACCTTGAACTGATGACCCCGG
P O P N I G F C S L L L C S W L E L L L G P
R S L T S E D S A V Y Y C A A G W N F D Y W G
A A H L R I L O S I I V O L V G T L T T S A

SEQ. ID. NO. 1
SEQ. ID. NO. 2
SEQ. ID. NO. 3
SEQ. ID. NO. 4
SEQ. ID. NO. 5

Alw26 I Dde I
AAGGCACCACTCTCACAGTCTCTCTCAGCCAAAACGACACCC 391
TTCCGTGGTGAGAGTGTACAGGAGTCCGTTTGTCTGTGGG
R H H S H S L L S Q N D T
O G T T L T V S S A K T T P
K A P L S O S P O P K R H P

FIGURE 7

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>115)	Seq2(1>125)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VH.PRO	MUVHIIA.PRO	75.6	2	10	125
(1>115)	(1>125)				

```

      10      20      30      40      50
EVQLQQSGPELVKPGTSVRISCKTSGYTFEYTI-HWVKQSHGKSLEWIGNINPNNGGTT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNNWVKOSPGKSLEWIGDINPGNGGTS
      10      20      30      40      50      60
^60      ^70      ^80      ^90      ^100      ^110
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGQGT
YNQKF :KATLTVDKSSSTAYM:L SLTSEDSAVYYCA G ...FDYWGQGT
YNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGT
      70      80      90      100      110      120

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LTVSS
 :TVSS
 VTVSS

FIGURE 8

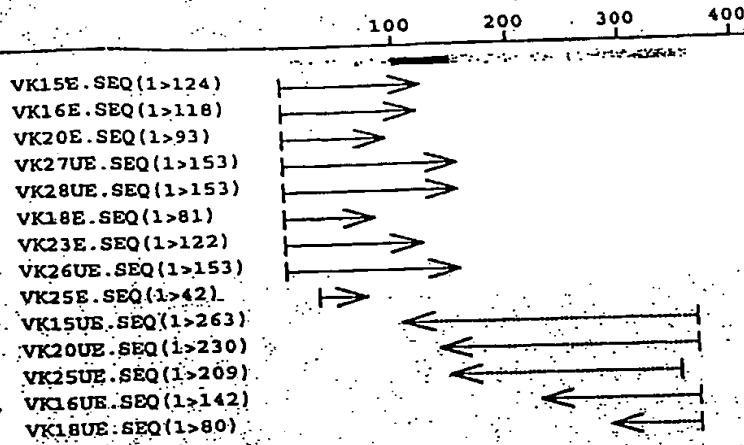


FIGURE 9

Enzymes: All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code

SEQ. ID. NO. 9 TTATATGGAGCTGATGGGAACATTGTAATGACCCAATCTCCAAATCCATGTCCATGTCACTAGGAGAGA 70
SEQ. ID. NO. 10 AATATACCTCGACTACCTTGTAACTTACTGGGTTAGAGGGTTTAGGTACAGGTACAGTCATCCTCTCT
SEQ. ID. NO. 11 L Y G A D G N I V M T O S P K S H S H S V G E
SEQ. ID. NO. 12 Y M E L M G T L P N L P N P C P C O E R
SEQ. ID. NO. 13 I I W S W E H C N D P I S O I H V H V S R R E

SEQ. ID. NO. 9 GGGTCACCTTGACCTGCAAGGCCAGTGAGAATGTGGTTACTTATGTTTCTGGTATCAACAGAAACCAGA 140
SEQ. ID. NO. 10 CCCAGTGGAACTGGACGTTCCGGTCACTCTTACACCAATGAATACAAAGGACCATAGTTGTCTTGGTCT
SEQ. ID. NO. 11 R V T L T C K A S E N V V T Y V S W Y O O K P E
SEQ. ID. NO. 12 G S P P A R P V R H W L L H F P G I N R N Q
SEQ. ID. NO. 13 G H L D L O G O E C G Y L C F L V S T E T R

SEQ. ID. NO. 9 GCAGTCTCCTAACTGCTGATATACGGGGCATCAACCGGTACACTGGGGTCCCCGATCGCTTCACAGGC 210
SEQ. ID. NO. 10 CGTCAGAGGATTGACCACTATATGCCCGTAGGTTGGCCATGTGACCCAGGGGCTAGCGAAGTGTCCG
SEQ. ID. NO. 11 O S P K L L I Y G A S N R Y T G V P D R F T G
SEQ. ID. NO. 12 S S L L N C Y T G H P T G T L G S P I A S Q A
SEQ. ID. NO. 13 A V S T A D I R G I O P V H W G P R S L H R

SEQ. ID. NO. 9 AGTGGATCTGCAACAGATTTCACTCTGACCATCAGCAGTGTGACGGCTGAAGACCTTGCAGATTATCACT 280
SEQ. ID. NO. 10 TCACCTAGACGTTGTCTAAAGTGAGACTGGTAGTCGTACACGTCGGACTTCTGGAACGTCTAATAGTGA
SEQ. ID. NO. 11 S G S A T O F T L T I S S V O A E D L A D Y H
SEQ. ID. NO. 12 V D L O O I S L P S A V C R L K T L O I I T
SEQ. ID. NO. 13 O W I C N R F H S O H O O C A G R P C R L S L

SEQ. ID. NO. 9 GTGGACAGGGTTACAGCTATCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGC 350
SEQ. ID. NO. 10 CACCTGTCCCAATGTCGATAGGCATGTGCAAGCCTCCCCCTGGTTCGACCTTTATTTTGGCCGACTACG
SEQ. ID. NO. 11 C G G G Y S Y P Y T F G G G T K L E I K R A D A
SEQ. ID. NO. 12 V D R V T A I R T R S E G G P S W K N G L M
SEQ. ID. NO. 13 W T G L O L S V H V R R G D O A G N K T G C

SEQ. ID. NO. 9 TGCACCAACTGTA 363
SEQ. ID. NO. 10 ACGTGGTTGACAT
SEQ. ID. NO. 11 A P T V
SEQ. ID. NO. 12 L H O L Y
SEQ. ID. NO. 13 C T N C

FIGURE 10

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>107)	Seq2(1>111)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VK.PRO	MUVKV.PRO	60.4	2	2	109
(1>107)	(1>109)				

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      10      20      30      40      50
NIVMTQSPKSMMSVGERVTLTCKAS-ENVVITYVSWYQOKPEQSPKLLIYGASNRYTGVP
:I MTQSP.S:S S:G:RVT:TC:AS :::Y::WYQOKP. SPKLLIY AS::GVP
DIOMTQSPSSLASLGDRVTITCRASODDISNYLNWYQOKPGGSPKLLIYYASRLHSGVP
      10      20      30      40      50      60
^60      ^70      ^80      ^90      ^100
DRFTGSGSATDFTLTISVQAEDLADYHCGGGYSY-PYTFGGGKLEIK
RE:GSGS:TD::LTIS:::ED:A.Y C. OG:: P TFGGGKLEIK
SRFSGSGSGTDYSLTISNLEQEDIATYFCQGGNTLPRTFGGGKLEIK
      70      80      90      100

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FIGURE 11